

SEQUENCE LISTING

<110> SHITARA, KENYA
 HOSAKA, EMI
 NATSUME, AKITO
 WAKITANI, MASAKO
 UCHIDA, KAZUHISA
 SATOH, MITSUO
 OHNUKI, NAOKO
 NAKAMAURA, KAZUYASU

<120> FUSED PROTEIN COMPOSITION

<130> BJS-249-426

<140> 10/575,261

<141> 2006-04-10

<150> PCT/JP04/15325

<151> 2004-10-08

<150> JP 2003-350158

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<170> PatentIn version 3.3

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<212> DNA

<213> Cricetulus griseus

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Gly Asp Lys Gly Lys Pro Arg Lys Val Ala Leu Ile Thr Gly Ile Thr	
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ggc cag gat ggc tca tac ttg gca gaa ttc ctg ctg gag aaa gga tac	144
Gly Gln Asp Gly Ser Tyr Leu Ala Glu Phe Leu Leu Glu Lys Gly Tyr	
35 40 45	
gag gtt cat gga att gta cgg cga tcc agt tca ttt aat aca ggt cga	192
Glu Val His Gly Ile Val Arg Arg Ser Ser Ser Phe Asn Thr Gly Arg	
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att gaa cat tta tat aag aat cca cag gct cat att gaa gga aac atg	240
Ile Glu His Leu Tyr Lys Asn Pro Gln Ala His Ile Glu Gly Asn Met	
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cat gtc aag att tcc ttt gac tta gca gag tac act gca gat gtt gat His Val Lys Ile Ser Phe Asp Leu Ala Glu Tyr Thr Ala Asp Val Asp 115 120 125	384
gga gtt ggc acc ttg cgg ctt ctg gat gca att aag act tgt ggc ctt Gly Val Gly Thr Leu Arg Leu Leu Asp Ala Ile Lys Thr Cys Gly Leu 130 135 140	432
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cat gag agt cct aga aga gga gct aat ttt gtt act cga aaa att agc His Glu Ser Pro Arg Arg Gln Ala Asn Phe Val Thr Arg Lys Ile Ser 210 215 220	672
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gga aat ctg gac gcc aaa cga gac tgg ggc cat gcc aag gac tat gtc Gly Asn Leu Asp Ala Lys Arg Asp Trp Gly His Ala Lys Asp Tyr Val 245 250 255	768
gag gct atg tgg ctg atg tta caa aat gat gaa cca gag gac ttt gtc Glu Ala Met Trp Leu Met Leu Gln Asn Asp Glu Pro Glu Asp Phe Val 260 265 270	816
ata gct act ggg gaa gtt cat agt gtc cgt gaa ttt gtt gag aaa tca Ile Ala Thr Gly Glu Val His Ser Val Arg Glu Phe Val Glu Lys Ser 275 280 285	864
ttc atg cac att gga aag acc att gtg tgg gaa gga aag aat gaa aat Phe Met His Ile Gly Lys Thr Ile Val Trp Glu Gly Lys Asn Glu Asn 290 295 300	912

gaa gtg ggc aga tgt aaa gag acc ggc aaa att cat gtg act gtg gat 960
 Glu Val Gly Arg Cys Lys Glu Thr Gly Lys Ile His Val Thr Val Asp
 305 310 315 320

ctg aaa tac tac cga cca act gaa gtg gac ttc ctg cag gga gac tgc 1008
 Leu Lys Tyr Tyr Arg Pro Thr Glu Val Asp Phe Leu Gln Gly Asp Cys
 325 330 335

tcc aag gcg cag cag aaa ctg aac tgg aag ccc cgc gtt gcc ttt gac 1056
 Ser Lys Ala Gln Gln Lys Leu Asn Trp Lys Pro Arg Val Ala Phe Asp
 340 345 350

gag ctg gtg agg gag atg gtg caa gcc gat gtg gag ctc atg aga acc 1104
 Glu Leu Val Arg Glu Met Val Gln Ala Asp Val Glu Leu Met Arg Thr
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 Asn Pro Asn Ala
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 <213> *Cricetulus griseus*

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Gly Gln Asp Gly Ser Tyr Leu Ala Glu Phe Leu Leu Glu Lys Gly Tyr
 35 40 45

Glu Val His Gly Ile Val Arg Arg Ser Ser Ser Phe Asn Thr Gly Arg
 50 55 60

Ile Glu His Leu Tyr Lys Asn Pro Gln Ala His Ile Glu Gly Asn Met
 65 70 75 80

Lys Leu His Tyr Gly Asp Leu Thr Asp Ser Thr Cys Leu Val Lys Ile
85 90 95

Ile Asn Glu Val Lys Pro Thr Glu Ile Tyr Asn Leu Gly Ala Gln Ser
100 105 110

His Val Lys Ile Ser Phe Asp Leu Ala Glu Tyr Thr Ala Asp Val Asp
115 120 125

Gly Val Gly Thr Leu Arg Leu Leu Asp Ala Ile Lys Thr Cys Gly Leu
130 135 140

Ile Asn Ser Val Lys Phe Tyr Gln Ala Ser Thr Ser Glu Leu Tyr Gly
145 150 155 160

Lys Val Gln Glu Ile Pro Gln Lys Glu Thr Thr Pro Phe Tyr Pro Arg
165 170 175

Ser Pro Tyr Gly Ala Ala Lys Leu Tyr Ala Tyr Trp Ile Val Val Asn
180 185 190

Phe Arg Glu Ala Tyr Asn Leu Phe Ala Val Asn Gly Ile Leu Phe Asn
195 200 205

His Glu Ser Pro Arg Arg Gly Ala Asn Phe Val Thr Arg Lys Ile Ser
210 215 220

Arg Ser Val Ala Lys Ile Tyr Leu Gly Gln Leu Glu Cys Phe Ser Leu
225 230 235 240

Gly Asn Leu Asp Ala Lys Arg Asp Trp Gly His Ala Lys Asp Tyr Val
245 250 255

Glu Ala Met Trp Leu Met Leu Gln Asn Asp Glu Pro Glu Asp Phe Val
260 265 270

Ile Ala Thr Gly Glu Val His Ser Val Arg Glu Phe Val Glu Lys Ser
275 280 285

Phe Met His Ile Gly Lys Thr Ile Val Trp Glu Gly Lys Asn Glu Asn
290 295 300

Glu Val Gly Arg Cys Lys Glu Thr Gly Lys Ile His Val Thr Val Asp
 305 310 315 320

Leu Lys Tyr Tyr Arg Pro Thr Glu Val Asp Phe Leu Gln Gly Asp Cys
 325 330 335

Ser Lys Ala Gln Gln Lys Leu Asn Trp Lys Pro Arg Val Ala Phe Asp
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Glu Leu Val Arg Glu Met Val Gln Ala Asp Val Glu Leu Met Arg Thr
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Asn Pro Asn Ala
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 <213> Cricetulus griseus

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 Leu Pro Gly Glu Glu Trp Val Phe Val Ser Ser Lys Asp Ala Asp Leu
 35 40 45
 Thr Asp Ala Ala Gln Thr Gln Ala Leu Phe Gln Lys Val Gln Pro Thr
 50 55 60
 His Val Ile His Leu Ala Ala Met Val Gly Gly Leu Phe Arg Asn Ile
 65 70 75 80
 Lys Tyr Asn Leu Asp Phe Trp Arg Lys Asn Val His Ile Asn Asp Asn
 85 90 95
 Val Leu His Ser Ala Phe Glu Val Gly Thr Arg Lys Val Val Ser Cys
 100 105 110
 Leu Ser Thr Cys Ile Phe Pro Asp Lys Thr Thr Tyr Pro Ile Asp Glu
 115 120 125
 Thr Met Ile His Asn Gly Pro Pro His Ser Ser Asn Phe Gly Tyr Ser
 130 135 140
 Tyr Ala Lys Arg Met Ile Asp Val Gln Asn Arg Ala Tyr Phe Gln Gln
 145 150 155 160

His Gly Cys Thr Phe Thr Ala Val Ile Pro Thr Asn Val Phe Gly Pro
 165 170 175

His Asp Asn Phe Asn Ile Glu Asp Gly His Val Leu Pro Gly Leu Ile
 180 185 190

His Lys Val His Leu Ala Lys Ser Asn Gly Ser Ala Leu Thr Val Trp
 195 200 205

Gly Thr Gly Lys Pro Arg Arg Gln Phe Ile Tyr Ser Leu Asp Leu Ala
 210 215 220

Arg Leu Phe Ile Trp Val Leu Arg Glu Tyr Asn Glu Val Glu Pro Ile
 225 230 235 240

Ile Leu Ser Val Gly Glu Glu Asp Glu Val Ser Ile Lys Glu Ala Ala
 245 250 255

Glu Ala Val Val Glu Ala Met Asp Phe Cys Gly Glu Val Thr Phe Asp
 260 265 270

Ser Thr Lys Ser Asp Gly Gln Tyr Lys Lys Thr Ala Ser Asn Gly Lys
 275 280 285

Leu Arg Ala Tyr Leu Pro Asp Phe Arg Phe Thr Pro Phe Lys Gln Ala
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<212> DNA

<213> *Cricetulus griseus*

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cctacatatc ctgaagctga aaaatagaga tggagtgtaa gagattaaca acagaattta	1860
gttcagacca tctcagccaa gcagaagacc cagactaaca tatggttcat tgacagacat	1920
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2008

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<213> *Cricetulus griseus*

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Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
 35 40 45

Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
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Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr
 65 70 75 80

Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
 85 90 95

Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Asp Leu Gly Lys Asp His
 100 105 110

Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
 115 120 125

Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Lys Leu Glu Gly Asn Glu
 130 135 140

Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu
 145 150 155 160

Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
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Gly Glu Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
 180 185 190

Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
 195 200 205

Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
 210 215 220

His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
 225 230 235 240

Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
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Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
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Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val
 275 280 285

Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
 290 295 300

Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Leu Arg Val His
 305 310 315 320

Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
 325 330 335

Arg Pro Gln Pro Trp Leu Glu Arg Glu Ile Glu Glu Thr Thr Lys Lys
 340 345 350

Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
 355 360 365

Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
 370 375 380

His Val Glu Glu His Phe Gln Leu Leu Glu Arg Arg Met Lys Val Asp
 385 390 395 400

Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ser Leu Leu Lys Glu
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Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
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Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
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Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
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Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
 465 470 475 480

Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
 485 490 495

Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
 500 505 510

His Gln Pro Arg Thr Lys Glu Glu Ile Pro Met Glu Pro Gly Asp Ile
 515 520 525

Ile Gly Val Ala Gly Asn His Trp Asn Gly Tyr Ser Lys Gly Val Asn
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<212> PRT

<213> Mus musculus

<400> 8

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Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
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 50 55 60

Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr
 65 70 75 80

Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
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Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Gly Leu Gly Lys Asp His
 100 105 110

Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
 115 120 125

Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys His Leu Glu Gly Asn Glu
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Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu
 145 150 155 160

Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
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Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
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Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
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Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
 210 215 220

His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
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Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
 245 250 255

Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
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Ser Thr Gly His Trp Ser Gly Glu Val Asn Asp Lys Asn Ile Gln Val
 275 280 285

Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
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Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Leu Arg Val His
 305 310 315 320

Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
 325 330 335

Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
 340 345 350

Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
 355 360 365

Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
 370 375 380

His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
 385 390 395 400

Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Thr Leu Leu Lys Glu
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Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
 420 425 430

Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
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Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
 450 455 460

Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
 465 470 475 480

Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
 485 490 495

Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
 500 505 510

His Lys Pro Arg Thr Glu Glu Glu Ile Pro Met Glu Pro Gly Asp Ile
 515 520 525

Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Ile Asn
 530 535 540

Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
 545 550 555 560

Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
 565 570 575

<210> 9
 <211> 5
 <212> PRT
 <213> Mus musculus

<400> 9
 Asp His Ala Ile His
 1 5

<210> 10
 <211> 17
 <212> PRT
 <213> Mus musculus

<400> 10
 Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe Lys
 1 5 10 15

Gly

<210> 11
 <211> 6
 <212> PRT
 <213> Mus musculus

<400> 11
 Ser Leu Asn Met Ala Tyr
 1 5

<210> 12
 <211> 17
 <212> PRT
 <213> Mus musculus

<400> 12
 Lys Ser Ser Gln Ser Leu Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu
 1 5 10 15

Ala

<210> 13
 <211> 7
 <212> PRT
 <213> Mus musculus

<400> 13
 Trp Ala Ser Ala Arg Glu Ser
 1 5

<210> 14
 <211> 9
 <212> PRT
 <213> Mus musculus

<400> 14
 Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr
 1 5

<210> 15
 <211> 115
 <212> PRT
 <213> Mus musculus

<400> 15
 Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Val Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
 100 105 110

Val Ser Ser
 115

<210> 16

<211> 113

<212> PRT

<213> Mus musculus

<400> 16

Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Pro Val Ser Val Gly
 1 5 10 15

Glu Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
 20 25 30

Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ala Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser
 65 70 75 80

Ile Ser Ser Val Lys Thr Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
 85 90 95

Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Val Leu
 100 105 110

Lys

<210> 17

<211> 265

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic protein

<400> 17

Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser Val Thr Thr Gly
 1 5 10 15

Val His Ser Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys
 20 25 30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Asp His Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu
 50 55 60

Glu Trp Ile Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn
 65 70 75 80

Glu Arg Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95

Thr Ala Tyr Val Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

Tyr Phe Cys Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr
 115 120 125

Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 130 135 140

Gly Gly Gly Gly Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu
 145 150 155 160

Pro Val Ser Val Gly Glu Lys Val Thr Leu Ser Cys Lys Ser Ser Gln
 165 170 175

Ser Leu Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln
 180 185 190

Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ala
 195 200 205

Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
 210 215 220

Asp Phe Thr Leu Ser Ile Ser Ser Val Lys Thr Glu Asp Leu Ala Val
 225 230 235 240

Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly
 245 250 255

Thr Lys Leu Val Leu Lys Arg Ala Ala
 260 265

<210> 18
 <211> 463
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 18
 ccggaattcg acccctcacc atggaatgga gctgggtctt tctcttcttc ctgtcagtaa 60
 ctacaggtgt ccaactccag gttcagttgc agcagtctga cgctgagttg gtgaaacctg 120
 gggcttcagt gaagatttcc tgcaaggctt ctggctacac cttcactgac catgcaattc 180
 actgggtgaa acagaaccct gaacagggcc tgggaatggat tggatatttt tctcccgga 240
 atgatgattt taaatacaat gagaggttca agggcaaggc cacactgact gcagacaaat 300
 cctccagcac tgctacgtg cagctcaaca gcctgacatc tgaggattct gcagtgtatt 360
 tctgtaccag atccctgaat atggcctact ggggtcaagg aacctcagtc accgtctcct 420
 caggtggcgg aggcagcgga ggcggtggct ccggaactag tcc 463

<210> 19
 <211> 129
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 19
 ccggaattcg acccctcacc atggaatgga gctgggtctt tctcttcttc ctgtcagtaa 60
 ctacaggtgt ccaactccag gttcagttgc agcagtctga cgctgagttg gtgaaacctg 120
 gggcttcagt 129

<210> 20
 <211> 134
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 20
 catttcgagg agaaaaatat ccaatccatt ccaggccctg ttcagggttc tgtttcaccc 60
 agtgaattgc atggtcagtg aagggttagc cagaagcctt gcaggaaatc ttcactgaag 120
 ccccagggtt cacc 134

<210> 21
 <211> 131
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 21
 ggatattttt ctcccggaaa tgatgatttt aaatacaatg agagggttcaa gggcaaggcc 60
 aactgactg cagacaaatc ctccagcact gcctacgtgc agctcaacag cctgacatct 120
 gaggattctg c 131

<210> 22
 <211> 132
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 22
 ggactagttc cggagccacc gcctccgtg cctccgccac ctgaggagac ggtgactgag 60
 gttccttgac ccagtaggc catattcagg gatctggtag agaaatacac tgcagaatcc 120
 tcagatgtca gg 132

<210> 23
 <211> 536
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 23

ccggaattct ccggaggcgg aggctcggac attgtgatgt cacagtctcc atcctcccta	60
cctgtgtcag ttggcgagaa gggtactttg agctgcaagt ccagtcagag ccttttatat	120
agtggtaatc aaaagaacta cttggcctgg taccagcaga aaccagggca gtctcctaaa	180
ctgctgattt actgggcacg cgctagggaa tctgggggtcc ctgatcgctt cacaggcagt	240
ggatctggga cagatttcac tctctccatc agcagtgtga agactgaaga cctggcagtt	300
tattactgtc agcagtatta tagctatccc ctcacgttcg gtgctgggac caagctggtg	360
ctgaaacggg ccgccgagcc caaatctcct gacaaaactc acacgtgccc accgtgcccc	420
gcacctgaac tcttgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc	480
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgac tagtcc	536

<210> 24

<211> 150

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 24

tctgaattct ccggaggcgg aggctcggac attgtgatgt cacagtctcc atcctcccta	60
cctgtgtcag ttggcgagaa gggtactttg agctgcaagt ccagtcagag ccttttatat	120
agtggtaatc aaaagaacta cttggcctgg	150

<210> 25

<211> 150

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 25

cacactgctg atggagagag tgaaatctgt ccagatcca ctgcctgtga agcgatcagg	60
gacccagat tcctagcgg atgccagta aatcagcagt ttaggagact gccttggttt	120
ctgctggtac caggccaagt agttcttttg	150

<210> 26
 <211> 149
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 26
 ctctctccat cagcagtgtg aagactgaag acctggcagt ttattactgt cagcagtatt 60
 atagctatcc cctcacgttc ggtgctggga ccaagctggg gctgaaacgg gccgccgagc 120
 ccaaattctcc tgacaaaact cacacgtgc 149

<210> 27
 <211> 149
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 27
 ggactagtca cgtccaccac cacgcatgtg acctcagggg tccgggagat catgagggtg 60
 tccttggggtt ttgggggggaa gaggaagact gacgggtcccc ccaggagtgc aggtgctggg 120
 cacgggtgggc acgtgtgagt tttgtcagg 149

<210> 28
 <211> 526
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 28
 caggaaacag ctatgacggt accgaattcg cgaggcaggc agcctggaga gaaggcgctg 60
 ggctgcgagg gcgcgagggc gcgagggcag ggggcaaccg gaccccgccc gcatccatgg 120
 cgcccgtcgc cgtctgggcc gcgctggccg tcggactgga gctctgggct gcggcgcacg 180
 ccttgcccgc ccagggtggca ttacaccct acgccccgga gcccgggagc acatgccggc 240
 tcagagaata ctatgaccag acagctcaga tgtgctgcag caaatgctcg ccgggccaac 300
 atgcaaaagt cttctgtacc aagacctcg acaccgtgtg tgactcctgt gaggacagca 360
 catacaccca gctctggaac tgggttcccc agtgcttgag ctgtgggtcc cgctgtagct 420

ctgaccagggt ggaaactcaa gcctgcactc gggaacagaa ccgcatctgc acctgcaggc 480
 ccggctggta ctgcgcgctg agcaagctta ctggccgctg ttttac 526

<210> 29
 <211> 537
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 29
 caggaaacag ctatgacggt accgctgagc aagcaggagg ggtgccggct gtgcgcgccg 60
 ctgcgcaagt gccgcccggg cttcggcgtg gccagaccag gaactgaaac atcagacgtg 120
 gtgtgcaagc cctgtgcccc ggggacgttc tccaacacga cttcatccac ggatatttgc 180
 agggcccacc agatctgtaa cgtggtggcc atccctggga atgcaagcat ggatgcagtc 240
 tgcacgtcca cgtccccac ccggagtatg gcccagggg cagtacactt accccagcca 300
 gtgtccacac gatcccaaca cacgcagcca actccagaac ccagcactgc tccaagcacc 360
 tccttctctg tcccaatggg cccagcccc ccagctgaag ggagcactgg cgacgagccc 420
 aaatcttctg acaaaaactca cacatgcca ccgtgcccag cacctgaact cctgggggga 480
 ccgtcagtct tcctcttccc cccaaaaccc aaggaagctt actggccgctc gttttac 537

<210> 30
 <211> 150
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 30
 atggcgcccc tcgccgtctg ggccgcgctg gccgtcggac tggagctctg ggctgcggcg 60
 cacgccttgc ccgcccagggt ggcatttaca ccctacgccc cggagcccgg gagcacatgc 120
 cggctcagag aatactatga ccagacagct 150

<210> 31
 <211> 135
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 31

agacggcgac gggcgccatg gatgcgggcg ggggccggtt gccccctgcc ctgcgcacct 60

cgcgcacctc cagcccagcg ccttctctcc aggtgcctg cctcgcgaat tcggtaccgt 120

catagctggt tcctg 135

<210> 32

<211> 150

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 32

gaactggggt cccgagtgt tgagctgtgg ctcccgtgt agctctgacc aggtggaaac 60

tcaagcctgc actcgggaac agaaccgcat ctgcacctgc aggcccggt ggtactgcgc 120

gctgagcaag cttactggcc gtcgttttac 150

<210> 33

<211> 150

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 33

gcactcggga acccagttcc agagctgggt gtatgtgctg tcctcacagg agtcacacac 60

gggtgtccgag gtcttggtac agaagacttt tgcattgttg cccggcgagc atttgctgca 120

gcacatctga gctgtctggt catagtattc 150

<210> 34

<211> 149

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 34

ctgtgccccg gggacgttct ccaacacgac ttcattccag gatatttgca ggccccacca 60

gatctgtaac gtggtggcca tccctgggaa tgcaagcatg gatgcagtct gcacgtccac 120
gtccccacc cggagtatgg ccccagggg 149

<210> 35
<211> 150
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 35
gaacgtcccc ggggcacagg gcttgcacac cacgtctgat gtttcagttc ctggtctggc 60
cacgccgaag cccggggcggc acttgccgag cggcgcgcac agccggcacc cctcctgctt 120
gctcagcggg accgtcatag ctgtttcctg 150

<210> 36
<211> 145
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 36
agctgaaggg agcactggcg acgagcccaa atcttgtgac aaaactcaca catgcccacc 60
gtgccagca cctgaactcc tggggggacc gtcagtcttc ctcttcccc caaaacccaa 120
ggaagcttac tggccgtcgt ttac 145

<210> 37
<211> 150
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 37
gccagtgtc ccttcagctg gggggctggg gccattggg agcaggaagg aggtgcttgg 60
agcagtgtc ggttctggag ttggctcgt gtgttgggat cgtgtggaca ctggctggg 120
taagtgtact gccctggg ccatactccg 150

<210> 38
 <211> 452
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 38
 caggaaacag ctatgacggt accgaattcc gacgagccat gggtgctggg agcgacgcgg 60
 ggcggggccct ggggggtcctc agcgtgggtct gcctgctgca ctgcttttggg ttcacacagct 120
 gttttttccca acaaatatat ggtggttgtgt atgggaatgt aactttccat gtaccaagca 180
 atgtgcctttt aaaagagggtc ctatggaaaa aacaaaagga taaagttgca gaactggaaa 240
 attctgaatt cagagctttc tcacttttta aaaatagggt ttatttagac actgtgtcag 300
 gtagcctcac tatctacaac ttaacatcat cagatgaaga tgagtatgaa atggaatcgc 360
 caaatattac tgataccatg aagttctttc tttatgtcga caaaactcac acatgcccac 420
 cgtgcccagc acctgactgg ccgtcgtttt ac 452

<210> 39
 <211> 138
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 39
 gtttcatcag ctgtttttcc caacaaatat atgggtgtgt gtatgggaat gtaactttcc 60
 atgtaccaag caatgtgcct ttaaaagagg tcctatggaa aaaacaaaag gataaagttg 120
 cagaactgga aaattctg 138

<210> 40
 <211> 129
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 40
 gggaaaaaca gctgatgaaa ccaaagcagt gcagcaggca gaccacgctg aggaccccca 60
 gggccccgcc cgcgctcgctc ccagcaacca tggctcgctc gaattcggtg ccgtcatagc 120

tgtttctg 129

<210> 41
 <211> 133
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 41
 cttaacatca tcagatgaag atgagtatga aatggaatcg ccaaata tta ctgataccat 60
 gaagttcttt ctttatgtcg acaaaactca cacatgccca ccgtgccag cacctgactg 120
 gcgctggttt tac 133

<210> 42
 <211> 118
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 42
 catcttcac tcgatgatgtt aagttgtaga tagtgaggct acctgacaca gtgtctaaat 60
 aaaccttatt tttaaaagat gagaaagctc tgaattcaga attttccagt tctgcaac 118

<210> 43
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 43
 gtaaacgac ggccagt 17

<210> 44
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 44
 taaatagaat tcggcatcat gtggcagctg ct 32

<210> 45
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 45
 aataaaggat cctgggggtca tttgtcttga ggggt 34

<210> 46
 <211> 788
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (13)..(774)

<400> 46
 gaattcggca tc atg tgg cag ctg ctc ctc cca act gct ctg cta ctt cta 51
 Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu
 1 5 10

gtt tca gct ggc atg cgg act gaa gat ctc cca aag gct gtg gtg ttc 99
 Val Ser Ala Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe
 15 20 25

ctg gag cct caa tgg tac agg gtg ctc gag aag gac agt gtg act ctg 147
 Leu Glu Pro Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu
 30 35 40 45

aag tgc cag gga gcc tac tcc cct gag gac aat tcc aca cag tgg ttt 195
 Lys Cys Gln Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe
 50 55 60

cac aat gag agc ctc atc tca agc cag gcc tcg agc tac ttc att gac 243
 His Asn Glu Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp
 65 70 75

gct gcc aca gtc gac gac agt gga gag tac agg tgc cag aca aac ctc 291
 Ala Ala Thr Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu
 80 85 90

tcc acc ctc agt gac ccg gtg cag cta gaa gtc cat atc ggc tgg ctg 339
 Ser Thr Leu Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu
 95 100 105

ttg ctc cag gcc cct cgg tgg gtg ttc aag gag gaa gac cct att cac	387
Leu Leu Gln Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His	
110 115 120 125	
ctg agg tgt cac agc tgg aag aac act gct ctg cat aag gtc aca tat	435
Leu Arg Cys His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr	
130 135 140	
tta cag aat ggc aaa ggc agg aag tat ttt cat cat aat tct gac ttc	483
Leu Gln Asn Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe	
145 150 155	
tac att cca aaa gcc aca ctc aaa gac agc ggc tcc tac ttc tgc agg	531
Tyr Ile Pro Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg	
160 165 170	
ggg ctt ttt ggg agt aaa aat gtg tct tca gag act gtg aac atc acc	579
Gly Leu Phe Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr	
175 180 185	
atc act caa ggt ttg gca gtg tca acc atc tca tca ttc ttt cca cct	627
Ile Thr Gln Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro	
190 195 200 205	
ggg tac caa gtc tct ttc tgc ttg gtg atg gta ctc ctt ttt gca gtg	675
Gly Tyr Gln Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val	
210 215 220	
gac aca gga cta tat ttc tct gtg aag aca aac att cga agc tca aca	723
Asp Thr Gly Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr	
225 230 235	
aga gac tgg aag gac cat aaa ttt aaa tgg aga aag gac cct caa gac	771
Arg Asp Trp Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp	
240 245 250	
aaa tgaccccgagg atcc	788
Lys	

<210> 47

<211> 254

<212> PRT

<213> Homo sapiens

<400> 47

Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Val Ser Ala
1 5 10 15

Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
20 25 30

Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
35 40 45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
 50 55 60

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
 65 70 75 80

Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
 85 90 95

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
 100 105 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
 115 120 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
 130 135 140

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
 145 150 155 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe
 165 170 175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
 180 185 190

Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln
 195 200 205

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
 210 215 220

Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp Trp
 225 230 235 240

Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
 245 250

<210> 48

<211> 788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13)..(774)

<400> 48

gaattcggca tc atg tgg cag ctg ctc ctc cca act gct ctg cta ctt cta	51
Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu	
1 5 10	
gtt tca gct ggc atg cgg act gaa gat ctc cca aag gct gtg gtg ttc	99
Val Ser Ala Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe	
15 20 25	
ctg gag cct caa tgg tac agg gtg ctc gag aag gac agt gtg act ctg	147
Leu Glu Pro Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu	
30 35 40 45	
aag tgc cag gga gcc tac tcc cct gag gac aat tcc aca cag tgg ttt	195
Lys Cys Gln Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe	
50 55 60	
cac aat gag agc ctc atc tca agc cag gcc tcg agc tac ttc att gac	243
His Asn Glu Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp	
65 70 75	
gct gcc aca gtc gac gac agt gga gag tac agg tgc cag aca aac ctc	291
Ala Ala Thr Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu	
80 85 90	
tcc acc ctc agt gac ccg gtg cag cta gaa gtc cat atc ggc tgg ctg	339
Ser Thr Leu Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu	
95 100 105	
ttg ctc cag gcc cct cgg tgg gtg ttc aag gag gaa gac cct att cac	387
Leu Leu Gln Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His	
110 115 120 125	
ctg agg tgt cac agc tgg aag aac act gct ctg cat aag gtc aca tat	435
Leu Arg Cys His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr	
130 135 140	
tta cag aat ggc aaa ggc agg aag tat ttt cat cat aat tct gac ttc	483
Leu Gln Asn Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe	
145 150 155	
tac att cca aaa gcc aca ctc aaa gac agc ggc tcc tac ttc tgc agg	531
Tyr Ile Pro Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg	
160 165 170	
ggg ctt gtt ggg agt aaa aat gtg tct tca gag act gtg aac atc acc	579
Gly Leu Val Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr	
175 180 185	
atc act caa ggt ttg gca gtg tca acc atc tca tca ttc ttt cca cct	627
Ile Thr Gln Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro	
190 195 200 205	

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 Gly Tyr Gln Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val
 210 215 220
 gac aca gga cta tat ttc tct gtg aag aca aac att cga agc tca aca 723
 Asp Thr Gly Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr
 225 230 235
 aga gac tgg aag gac cat aaa ttt aaa tgg aga aag gac cct caa gac 771
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 <211> 254
 <212> PRT
 <213> Homo sapiens

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 35 40 45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
 50 55 60

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
 65 70 75 80

Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
 85 90 95

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
 100 105 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
 115 120 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
 130 135 140

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
 145 150 155 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val
 165 170 175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
 180 185 190

Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln
 195 200 205

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
 210 215 220

Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp Trp
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Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
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<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

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<211> 620

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<213> Homo sapiens

<220>

<221> CDS

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51

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 Val Ser Ala Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe
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ctg gag cct caa tgg tac agg gtg ctc gag aag gac agt gtg act ctg 147
 Leu Glu Pro Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu
 30 35 40 45

aag tgc cag gga gcc tac tcc cct gag gac aat tcc aca cag tgg ttt 195
 Lys Cys Gln Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe
 50 55 60

cac aat gag agc ctc atc tca agc cag gcc tcg agc tac ttc att gac 243
 His Asn Glu Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp
 65 70 75

gct gcc aca gtc gac gac agt gga gag tac agg tgc cag aca aac ctc 291
 Ala Ala Thr Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu
 80 85 90

tcc acc ctc agt gac ccg gtg cag cta gaa gtc cat atc ggc tgg ctg 339
 Ser Thr Leu Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu
 95 100 105

ttg ctc cag gcc cct cgg tgg gtg ttc aag gag gaa gac cct att cac 387
 Leu Leu Gln Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His
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 Leu Arg Cys His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr
 130 135 140

tta cag aat ggc aaa ggc agg aag tat ttt cat cat aat tct gac ttc 483
 Leu Gln Asn Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe
 145 150 155

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 Tyr Ile Pro Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg
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 Gly Leu Phe Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr
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<210> 52

<211> 199

<212> PRT

<213> Homo sapiens

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Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
35 40 45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
50 55 60

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
65 70 75 80

Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
85 90 95

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
100 105 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
115 120 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
130 135 140

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
145 150 155 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe
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180 185 190

Gly His His His His His His
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Val Ser Ala Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe	
15 20 25	
ctg gag cct caa tgg tac agg gtg ctc gag aag gac agt gtg act ctg	147
Leu Glu Pro Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu	
30 35 40 45	
aag tgc cag gga gcc tac tcc cct gag gac aat tcc aca cag tgg ttt	195
Lys Cys Gln Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe	
50 55 60	
cac aat gag agc ctc atc tca agc cag gcc tcg agc tac ttc att gac	243
His Asn Glu Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp	
65 70 75	
gct gcc aca gtc gac gac agt gga gag tac agg tgc cag aca aac ctc	291
Ala Ala Thr Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu	
80 85 90	
tcc acc ctc agt gac ccg gtg cag cta gaa gtc cat atc ggc tgg ctg	339
Ser Thr Leu Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu	
95 100 105	
ttg ctc cag gcc cct cgg tgg gtg ttc aag gag gaa gac cct att cac	387
Leu Leu Gln Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His	
110 115 120 125	
ctg agg tgt cac agc tgg aag aac act gct ctg cat aag gtc aca tat	435
Leu Arg Cys His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr	
130 135 140	
tta cag aat ggc aaa ggc agg aag tat ttt cat cat aat tct gac ttc	483
Leu Gln Asn Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe	
145 150 155	
tac att cca aaa gcc aca ctc aaa gac agc ggc tcc tac ttc tgc agg	531
Tyr Ile Pro Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg	
160 165 170	
ggg ctt gtt ggg agt aaa aat gtg tct tca gag act gtg aac atc acc	579
Gly Leu Val Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr	
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<210> 54
 <211> 199
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 <213> Homo sapiens

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Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala
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Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
 20 25 30

Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
 35 40 45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
 50 55 60

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
 65 70 75 80

Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
 85 90 95

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
 100 105 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
 115 120 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
 130 135 140

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
 145 150 155 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val
 165 170 175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
 180 185 190

Gly His His His His His His
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<210> 55
 <211> 9196
 <212> DNA
 <213> *Cricetulus griseus*

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tcataaacct	ggggaatagt	gctaccacaa	tgggcatatc	cacttacttc	agttcatgca	7080
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ccagatgatt	agactgtgtc	aagttgacaa	ttaaaactat	cacacctgaa	gccatcacta	7200
gtaaatataa	tgaaaatggt	gattatcacc	ataattcato	tgtatccctt	tgttattgta	7260
gattttgtga	agttcctatt	caagtccttg	ttccttcctt	aaaaacctgt	tttttagtta	7320
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aggaaggggtg	aggccctcca	tgggggaaat	cttcaatgtc	tgtcatatca	tttggagcag	7620
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 caggtgatgc caacttttaa tggttaccag tggataagag tgcttgatc tctagacccc 9120
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 aggatcccaa gagctc 9196

<210> 56
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 56
 gagacttcag cccacttcaa ttattggc 28

<210> 57
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 57
 cttgtgtgac tcttaactct cagag 25

<210> 58
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 58
 gaggccactt gtgtagcgcc aagtg 25

<210> 59
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 59
 ccctcgagat aacttcgtat agc 23

<210> 60
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 60
 ggtaggcctc actaactg 18

<210> 61
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 61
 catagaaaca agtaacaaca gccag 25

<210> 62
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 62
 gtgagtccat ggctgtcact g 21

<210> 63
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 63
 cctgacttgg ctattctcag

20

<210> 64
 <211> 235
 <212> PRT
 <213> Homo sapiens

<400> 64
 Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
 1 5 10 15

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
 20 25 30

Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
 35 40 45

Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
 50 55 60

Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
 65 70 75 80

Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
 85 90 95

Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
 100 105 110

Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
 115 120 125

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
 130 135 140

46

Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
145 150 155 160

Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
165 170 175

Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
180 185 190

His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
195 200 205

Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
210 215 220

Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp
225 230 235

<210> 65

<211> 92

<212> PRT

<213> Homo sapiens

<400> 65

Phe Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His
1 5 10 15

Val Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys
20 25 30

Asp Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser
35 40 45

Phe Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile
50 55 60

Tyr Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro
65 70 75 80

Asn Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val
85 90

<210> 66

<211> 5

<212> PRT

<213> Mus musculus

<400> 66
 Ser Tyr Gly Met Ser
 1 5

<210> 67
 <211> 17
 <212> PRT
 <213> Mus musculus

<400> 67
 Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys
 1 5 10 15

Gly

<210> 68
 <211> 11
 <212> PRT
 <213> Mus musculus

<400> 68
 Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr
 1 5 10

<210> 69
 <211> 10
 <212> PRT
 <213> Mus musculus

<400> 69
 Ser Ala Ser Ser Ser Val Ser Tyr Met His
 1 5 10

<210> 70
 <211> 7
 <212> PRT
 <213> Mus musculus

<400> 70
 Asp Thr Ser Lys Leu Ala Ser
 1 5

<210> 71
 <211> 9
 <212> PRT
 <213> Mus musculus

<400> 71
 Gln Gln Trp Ser Ser Asn Pro Pro Thr
 1 5

<210> 72
 <211> 120
 <212> PRT
 <213> Mus musculus

<400> 72
 Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Leu Val
 35 40 45
 Ala Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr Trp Gly Pro
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 73
 <211> 109
 <212> PRT
 <213> Mus musculus

<400> 73
 Asp Ile Glu Leu Thr Gln Ser Pro Ser Ile Met Ser Ala Ser Pro Gly
 1 5 10 15
 Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Pro Thr
85 90 95

Phe Gly Gly Arg Thr Lys Leu Glu Leu Lys Arg Ala Ala
100 105

<210> 74

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein

<400> 74

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Leu Val
35 40 45

Ala Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr Trp Gly Pro
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

50

Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ser
130 135 140

Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr
165 170 175

Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Trp Ser Ser Asn Pro Pro Thr Phe Gly Gly Arg Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala

<210> 75

<211> 515

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein

<400> 75

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Leu Val
35 40 45

Ala Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr Trp Gly Pro
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ser
130 135 140

Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr
165 170 175

Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Trp Ser Ser Asn Pro Pro Thr Phe Gly Gly Arg Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
245 250 255

Gly Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln
260 265 270

Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys
275 280 285

Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His Ala Ile His
290 295 300

Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile Gly Tyr Phe
305 310 315 320

Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe Lys Gly Lys
325 330 335

Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Val Gln Leu
340 345 350

Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Thr Arg Ser
355 360 365

Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
385 390 395 400

Ile Val Met Ser Gln Ser Pro Ser Ser Leu Pro Val Ser Val Gly Glu
405 410 415

Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser Gly
420 425 430

Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser
435 440 445

Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ala Arg Glu Ser Gly Val Pro
450 455 460

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile
465 470 475 480

Ser Ser Val Lys Thr Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln Tyr
485 490 495

Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Val Leu Lys
500 505 510

Arg Ala Ala
515

<210> 76

<211> 515

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein

<400> 76

Gln	Val	Gln	Leu	Gln	Gln	Ser	Asp	Ala	Glu	Leu	Val	Lys	Pro	Gly	Ala
1			5						10					15	

Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	His
		20						25					30		

Ala	Ile	His	Trp	Val	Lys	Gln	Asn	Pro	Glu	Gln	Gly	Leu	Glu	Trp	Ile
		35					40					45			

Gly	Tyr	Phe	Ser	Pro	Gly	Asn	Asp	Asp	Phe	Lys	Tyr	Asn	Glu	Arg	Phe
	50					55					60				

Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
65					70					75					80

Val	Gln	Leu	Asn	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
			85						90					95	

Thr	Arg	Ser	Leu	Asn	Met	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr
			100					105						110	

Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
		115					120					125			

Gly	Ser	Asp	Ile	Val	Met	Ser	Gln	Ser	Pro	Ser	Ser	Leu	Pro	Val	Ser
	130					135					140				

Val	Gly	Glu	Lys	Val	Thr	Leu	Ser	Cys	Lys	Ser	Ser	Gln	Ser	Leu	Leu
145					150					155					160

Tyr	Ser	Gly	Asn	Gln	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro
			165						170					175	

Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Ala	Arg	Glu	Ser
			180					185					190		

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
 195 200 205

Leu Ser Ile Ser Ser Val Lys Thr Glu Asp Leu Ala Val Tyr Tyr Cys
 210 215 220

Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
 225 230 235 240

Val Leu Lys Arg Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 245 250 255

Gly Gly Gly Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
 260 265 270

Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
 275 280 285

Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly
 290 295 300

Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Leu Val Ala
 305 310 315 320

Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys
 325 330 335

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
 340 345 350

Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala
 355 360 365

Arg Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr Trp Gly Pro Gly
 370 375 380

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 385 390 395 400

Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ser Ile
 405 410 415

Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser
 420 425 430

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser
 435 440 445

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro
 450 455 460

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 465 470 475 480

Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 485 490 495

Ser Ser Asn Pro Pro Thr Phe Gly Gly Arg Thr Lys Leu Glu Leu Lys
 500 505 510

Arg Ala Ala
 515

<210> 77
 <211> 89
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 77
 gaattcgacc cctcaccatg gaatggagct gggctctttct cttcttctctg tcagtaacta 60
 ccggtgggga tccccactag tcctccgga 89

<210> 78
 <211> 83
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 78
 aattcgaccc ctcaccatgg aatggagctg ggtctttctc ttcttctctg cagtaactac 60
 cggtggggat cccactagt cct 83

<210> 79
 <211> 83
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 79
 ccggaggact agtggggatc cccaccggtg gttactgaca ggaagaagag aaagaccag 60
 ctccattcca tgggtgagggg tcg 83

<210> 80
 <211> 411
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 80
 gcgaccggtg tccactccca ggtccaactg caggagtcag gaggaggctt agtgcagcct 60
 ggagggtccc tgaaactctc ctgtgcagcc tctggattca ctttcagtag ctatggcatg 120
 tcttggttcc gccagactcc agacaagagg ctggagttgg tcgcaaccat taatagtaat 180
 ggtggttagca cctattatcc agacagtgtg aagggccgat tcaccatctc cagagacaat 240
 gccagaaca ccctgtacct gcaaagtgc agtctgaagt ctgaggacac agccatgtat 300
 tactgtgcaa gagatcggga tggttacgac gagggatttg actactgggg cccagggacc 360
 acggtcaccg tctcctcagg tggcggaggc agcggaggcg gtggatcccg c 411

<210> 81
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 81
 gcgaccggtg tccactccca ggtccaactg caggagtcag gaggaggctt agtgcagcct 60
 ggagggtccc tgaaactctc ctgtgcagcc tctggattca ctttcagtag ctatggcatg 120

<210> 82
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 82
 cggcccttca cactgtcttg ataatagggt ctaccacat tactattaat ggttgcgacc 60
 aactccagcc tcttgtcttg agtctggcga acccaagaca tgccatagct actgaaagtg 120

<210> 83
 <211> 118
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 83
 ccagacagt tgaagggccg attcaccatc tccagagaca atgccaagaa caccctgtac 60
 ctgcaaata gcaagtctgaa gtctgaggac acagccatgt attactgtgc aagagatc 118

<210> 84
 <211> 118
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 84
 cgcggatcca ccgcctccgc tgcctccgcc acctgaggag acggtgaccg tggtccttg 60
 gccccagtag tcaaatacct cgtcgtaacc atcccgatct cttgcacagt aatacatg 118

<210> 85
 <211> 386
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 85
 gcgggatccg gtggcggagg ctccgacatt gagtgaccc aatctccatc aatcatgtct 60
 gcatctccag gggagaaggt caccatgacc tgcagtgcc gctcaagtgt aagttacatg 120

cactgggtacc agcagaagtc aggcacctcc cccaaaagat ggatttatga cacatccaaa 180
 ctggcttctg gagtccctgc tcgcttcagt ggagtggggt ctgggacctc ttactctctc 240
 acaatcagca gcatggaggc tgaagatgct gccacttatt actgccagca gtggagtagt 300
 aaccacacca cggttcggagg gcggaccaag ctggaactga aacggggccgc cgagcccaaa 360
 tctcctgaca aaactcacac gtggcg 386

<210> 86
 <211> 109
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 86
 gcgggatccg gtggcggagg ctggacatt gagctgacct aatctccatc aatcatgtct 60
 gcatctccag gggagaaggc caccatgacc tgcagtgccg gctcaagtg 109

<210> 87
 <211> 111
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 87
 gcagggactc cagaagccag tttggatgtg tcataaatcc atcttttggg ggaggtgcct 60
 gacttctgct ggtaccagtg catgtaactt acacttgagc tggcactgca g 111

<210> 88
 <211> 114
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 88
 ctggcttctg gagtccctgc tcgcttcagt ggagtggggt ctgggacctc ttactctctc 60
 acaatcagca gcatggaggc tgaagatgct gccacttatt actgccagca gtgg 114

<210> 89
 <211> 114
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 89
 cgccacgtgt gagttttgtc aggagatttg ggctcggcgg cccgtttcag ttccagcttg 60
 gtccgccttc cgaacgtggg tgggttacta ctccactgct ggcagtaata agtg 114

<210> 90
 <211> 399
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 90
 gcgggatccg gtggcggagg ctccgacatt gagctgacct aatctccatc aatcatgtct 60
 gcatctccag gggagaaggt caccatgacc tgcaagtgt aagttacatg 120
 cactggtacc agcagaagtc aggcacctcc cccaaaagat ggatttatga cacatccaaa 180
 ctggcttctg gagtcctgc tcgcttcagt ggcagtgggt ctgggacctc ttactctctc 240
 acaatcagca gcatggaggc tgaagatgct gccacttatt actgccagca gtggagtagt 300
 aaccaccca cgttcggagg gcggaccaag ctggaactga aacggggccgc cgggtggcgga 360
 ggcagcggag gcggtggtag cggtggcgga actagtgcg 399

<210> 91
 <211> 127
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 91
 cgcactagtt ccgccaccgc taccaccgcc tccgtgcct ccgccaccgg cggcccgttt 60
 cagttccagc ttggtccgcc ctccgaacgt ggggtgggtta ctactccact gctggcagta 120
 ataagtg 127

<210> 92
 <211> 812
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 92
 tttagtagtg gtggcggagg cagcggaggc ggtggtagcc aggttcagtt gcagcagttct 60
 gacgctgagt tgggtgaaacc tggggcttca gtgaagatatt cctgcaaggc ttctggctac 120
 accttcactg accatgcaat tcactgggtg aaacagaacc ctgaacaggg cctggaatgg 180
 attggatatt tttctcccg aaatgatgat tttaaatata atgagagggt caagggcaag 240
 gccacactga ctgcagacaa atcctccagc actgcctacg tgcagctcaa cagcctgaca 300
 tctgaggatt ctgcagtgt tttctgtacc agatccctga atatggccta ctgggggtcaa 360
 ggaacctcag tcaccgtctc ctccaggtggc ggaggcagcg gaggcggtgg ctccggaggc 420
 ggaggctcgg acattgtgat gtcacagtct ccctccctcc tacctgtgtc agttggcgag 480
 aagggttactt tgagctgcaa gtccagtcag agccttttat atagtggtaa tcaaaagaac 540
 tacttggcct ggtaccagca gaaaccaggg cagtctccta aactgctgat ttactgggca 600
 tccgctaggg aatctgggggt ccctgatcgc ttcacaggca gtggatctgg gacagatttc 660
 actctctcca tcagcagtgt gaagactgaa gacctggcag tttattactg tcagcagtat 720
 tatagctatc ccctcacgtt cgggtgctggg accaagctgg tgctgaaacg ggccgccgag 780
 cccaaatctc ctgacaaaac tcacacgtgc cc 812

<210> 93
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 93
 tttagtagtg gtggcggagg cagcggaggc ggtggtagcc aggttcagtt gcagcagttct 60
 gacg 64

<210> 94
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 94

gggcacgtgt gagttttgtc agg

23

<210> 95

<211> 817

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 95

cttcctgtca gtaactaccg gtgtccactc ccagggttcag ttgcagcagt ctgacgctga	60
gttggtgaaa cctggggcctt cagtgaagat ttcttgcaag gcttctggct acaccttcac	120
tgaccatgca attcactggg tgaaacagaa ccctgaacag ggcctggaat ggattggata	180
tttttctccc ggaaatgatg attttaaata caatgagagg ttcaagggca aggccacact	240
gactgcagac aaatcctcca gcactgccta cgtgcagctc aacagcctga catctgagga	300
ttctgcagtg tatttctgta ccagatccct gaatatggcc tactggggtc aaggaacctc	360
agtcaccgtc tcttcaggtg gcgaggcag cggaggcgtt ggctccggag gcgagggtc	420
ggacattgtg atgtcacagt ctccatcctc cctacctgtg tcagttggcg agaaggttac	480
tttgagctgc aagtcagtc agagcctttt atatagtggc aatcaaaaga actacttggc	540
ctggtaccag cagaaaccag ggcagtctcc taaactgctg atttactggg catccgctag	600
ggaatctggg gtccctgata gcttcacagg cagtggatct gggacagatt tcaactcttc	660
catcagcagt gtgaagactg aagacctggc agtttattac tgtcagcagt attatagcta	720
tcccctcacg ttcggtgctg ggaccaagct ggtgctgaaa cgggccgccg gtggcgagg	780
cagcggaggc ggtggtagcg gtggcggaac tagtaaa	817

<210> 96

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 96
cttcctgtca gtaactaccg gtgtccactc ccaggttcag 40

<210> 97
<211> 85
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 97
tttactagtt ccgccaccgc taccaccgcc tccgctgcct ccgccaccgg cggcccgttt 60
cagcaccagc ttggtcccag caccg 85

<210> 98
<211> 806
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 98
tttactagtg gtggcggagg cagcggaggc ggtggtagcc aggtccaact gcaggagtca 60
ggaggaggct tagtgcagcc tggagggtcc ctgaaactct cctgtgcagc ctctggattc 120
actttcagta gctatggcat gtcttgggtt cgccagactc cagacaagag gctggagttg 180
gtcgcaacca ttaatagtaa tgggtgtagc acctattatc cagacagtgt gaagggccga 240
ttcaccatct ccagagacaa tgccaagaac acctgtacc tgcaaatgag cagtctgaag 300
tctgaggaca cagccatgta ttactgtgca agagatcggg atggttacga cgagggattt 360
gactactggg gcccagggac cacggtcacc gtctcctcag gtggcggagg cagcggaggc 420
ggtggatccg gtggcggagg ctcggaatt gagctgaccc aatctccatc aatcatgtct 480
gcatctccag gggagaaggc caccatgacc tgcaagtgt gctcaagtgt aagttacatg 540
cactggtacc agcagaagtc aggcacctcc cccaaaagat ggatttatga cacatccaaa 600
ctggcttctg gagtcctgc tcgcttcagt ggcagtgggt ctgggacctc ttactctctc 660
acaatcagca gcatggaggc tgaagatgct gccacttatt actgccagca gtggagtagt 720
aaccaccca cgttcggagg gcggaccaag ctggaactga aacgggccgc cgagcccaaa 780
tctcctgaca aaactcacac gtgcc 806

<210> 99
 <211> 65
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 99
 ttactagtgt gtggcggagg cagcggaggc ggtggtagcc aggtccaact gcaggagtca 60
 ggagg 65

<210> 100
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 100
 acaacggaat tcaagcctgt agcacatggt gtagc 35

<210> 101
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 101
 ggcgggatcc tcacagggca atgatcccaa agtagacct 39

<210> 102
 <211> 99
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 102
 aacaacggaa ttcgaccac ggctccacc tctctcccct ggaaaggaca ccatgagcac 60
 tgaaagcatg atccgggacg tggagctggc cgaggaggc 99

<210> 103
 <211> 99
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 103
 tgccacgatc aggaaggaga agaggctgag gaacaagcac cgcctggagc cctggggccc 60
 ccctgtcttc ttggggagcg cctcctcggc cagctccac 99

<210> 104
 <211> 99
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 104
 tctccttcct gatcgtggca ggcgccacca cgctcttctg cctgctgcac ttgggagtga 60
 tcggcccccga gaggggaagag ttccccaggg acctctctc 99

<210> 105
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 105
 ttggctacaa catgtgctac tgccctgggcc agagggctga ttagagagag gtccttgggg 60
 aac 63

<210> 106
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 106
 aacaacggaa ttcgaccac 20

<210> 107
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 107
 ttggctacaa catgtgctac

20

<210> 108
 <211> 717
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (46)..(708)

<400> 108
 gaattcgacc cacggctcca cctctctctcc cctggaaaagg acacc atg agc act gaa
 Met Ser Thr Glu
 1

57

agc atg atc cgg gac gtg gag ctg gcc gag gag gcg ctc ccc aag aag
 Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala Leu Pro Lys Lys
 5 10 15 20

105

aca ggg ggg ccc cag ggc tcc agg cgg tgc ttg ttc ctc agc ctc ttc
 Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe Leu Ser Leu Phe
 25 30 35

153

tcc ttc ctg atc gtg gca ggc gcc acc acg ctc ttc tgc ctg ctg cac
 Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe Cys Leu Leu His
 40 45 50

201

ttt gga gtg atc ggc ccc cag agg gaa gag ttc ccc agg gac ctc tct
 Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro Arg Asp Leu Ser
 55 60 65

249

cta atc agc cct ctg gcc cag gca gta gca cat gtt gta gca aac cct
 Leu Ile Ser Pro Leu Ala Gln Ala Val Ala His Val Val Ala Asn Pro
 70 75 80

297

caa gct gag ggg cag ctc cag tgg ctg aac cgc cgg gcc aat gcc ctc
 Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
 85 90 95 100

345

ctg gcc aat ggc gtg gag ctg aga gat aac cag ctg gtg gtg cca tca
 Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
 105 110 115

393

gag ggc ctg tac ctc atc tac tcc cag gtc ctc ttc aag ggc caa ggc 441
 Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
 120 125 130

tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc agc cgc atc gcc 489
 Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
 135 140 145

gtc tcc tac cag acc aag gtc aac ctc ctc tct gcc atc aag agc ccc 537
 Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
 150 155 160

tgc cag agg gag acc cca gag ggg gct gag gcc aag ccc tgg tat gag 585
 Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
 165 170 175 180

ccc atc tat ctg gga ggg gtc ttc cag ctg gag aag ggt gac cga ctc 633
 Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
 185 190 195

agc gct gag atc aat cgg ccc gac tat ctc gac ttt gcc gag tct ggg 681
 Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
 200 205 210

cag gtc tac ttt ggg atc att gcc ctg tgaggatcc 717
 Gln Val Tyr Phe Gly Ile Ile Ala Leu
 215 220

<210> 109

<211> 221

<212> PRT

<213> Homo sapiens

<400> 109

Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
 1 5 10 15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
 20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
 35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
 50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Ala His Val
 65 70 75 80

Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
 85 90 95

Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
 100 105 110

Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
 115 120 125

Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
 130 135 140

Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
 145 150 155 160

Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
 165 170 175

Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
 180 185 190

Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
 195 200 205

Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
 210 215 220

<210> 110

<211> 383

<212> DNA

<213> *Cricetulus griseus*

<400> 110

gttaactggg gctcttttaa accctgaatt tttctaaatc cccacctcca agagtttggt 60

ttaaactgat ttttttaatg aatacctttt gaagaataga gcattgtctc atcatgcaaa 120

gcttctcagg gattcagcta gcatgttgaa gaaacataag ggtgttaa at tgtttgtcac 180

aagtgttgaa taaatattga cgtagtcttc agctattcta tactggaagt agatgatatt 240

ctcattggaa attctgttag gaagtaacct ttcttgtctt cttacctgca tagaatccca 300

ggatataaaa cttgtgcttg tcgcccttgc cattgtctct cactggtggc ctttattgca 360

tctcatatct gccttctctt tcc 383

<210> 111

<211> 564

<212> DNA

<213> *Cricetulus griseus*

<400> 111
 taagaattcc tgtgcccagc tgtatgtgag gctctctgca ggtgtaggga tgtttctgct 60
 ttctttctgc acatgcttca cagctgaagt cttttgggtg tgagattgac attcagatag 120
 actaaagtga ctggacttgt tgggaaacat actgtatgca ttattgccgt tgcctccagg 180
 tgaaattaac acctcattca ccaatccctg ttcattccaaa ctttctaccc acatcacttt 240
 aatagaaat tagaccaat atgactcctt ttttctaag ctgtttatag agattgtgct 300
 ggagcagtga gcttttgtgt ttgtttgttt gttttgtaat tttcccatg aaaatttctc 360
 taaactcaaa cctaagaggg aaaaaaaaaa aacagactta tatgtgccac acttgtaaaa 420
 aaaaatcatg aaagatgtat atgatatttt taaacagttt gaatattaag atcacaattt 480
 ctatttttaa aacaatcttg ttttacatat caatcaccca attcccttgc cttcccatcc 540
 tcccatcccc cccactgac cccc 564

<210> 112
 <211> 120
 <212> DNA
 <213> *Cricetulus griseus*

<400> 112
 atgaatgttc attctttggg tatatgccca agagtagaat tgctaaatat tgaggtagac 60
 tgattcccat tttcttgagg agtcgccata ttgatttcca aagtgactgt acaagttaac 120

<210> 113
 <211> 274
 <212> DNA
 <213> *Cricetulus griseus*

<400> 113
 aggcactagg taaatatttt tgaagaaaga atgagtatct cctatttcag aaaaactttt 60
 attgacttaa atttaggata tcagaattag aaaacagtaa aaatttatag gagagtgttt 120
 aatgaatggt attttaagg tccatacaaa tagtaattaa aacttacaca aactatttgt 180
 agtaatgatt cagtctggta taccctgatg agcattatac actttttaa tctttttgta 240
 aattttttta ttagttcaaa ttaggaacaa gctt 274